Amendments to the Specification

Please replace the previous Sequence Listing with the new Sequence Listing submitted herewith.

Please replace Paragraph 50 with the following replacement paragraph.

[0050] Linkage of a TM to one or more imaging agents may be achieved by any means known to those in the art, such as genetic fusion, covalent chemical attachment, noncovalent attachment (*e.g.*, adsorption) or a combination of such means. Selection of a method for linking a TM to an imaging agent will vary depending, in part, on the chemical nature of the agent and depending on whether the agent is to function at the basolateral surface, within the epithelial cell, or undergo transcytosis. Linkage by genetic fusion may be performed using standard recombinant DNA techniques to generate a nucleic acid molecule that encodes a single fusion peptide containing both the imaging agent(s) and the TM. Optionally, a TM may also be linked to one or more linker sequences and/or sequences for intracellular targeting (*e.g.*, KDEL **(SEQ ID NO: 44)**, protease cleavage sites, etc.). Such sequences may be linked to a TM by genetic fusion using standard recombinant DNA techniques to generate a nucleic acid molecule encoding the TM and the desired additional sequences. The recombinant nucleic acid molecule is then introduced into an appropriate vector and expressed in suitable host cells. Techniques for generating such a recombinant molecule and expressing a fusion peptide are well known to those of ordinary skill in the art (*see, e.g.*, Sambrook et al., *Molecular Cloning: A Laboratory Manual,* 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). Any imaging agent having a known polypeptide sequence may be linked to a TM by genetic fusion.

Please replace Paragraph 54 with the following replacement paragraph.

[0054] These protease recognition sites are extremely useful in the design of scissile linkers enabling the delivery of imaging agents to the intracellular environment of epithelial cells or to the epithelial barrier in general. Delivery of such compounds to epithelial cells can be

accomplished by using residues 585-600 of human pIgR (SEQ ID NO:45) or residues 30-40 of procathepsin E (SEQ ID NO:39) as part of the scissile linker joining the imaging agent to TM. Alternatively, scissile linkers may be designed from other cancer cell specific or epithelial barrier specific processing proteases which may be identified by the comparison of newly synthesized and secreted proteins or similar techniques. Other types of proteases that can be used to cleave scissile bonds can be found in the mammalian duodenum, for example. The enterokinase recognition sequence, $(Asp)_4$-lys **(residues 3-6 OF SEQ ID NO: 26)**, can be used as a scissile linker for delivery of imaging agents to the duodenum by TM mediated transcytosis across the duodenum epithelial barrier.

Please replace Paragraph 100 with the following replacement paragraph.

[0100] Assembly of D1.1 and insertion into the TM synthetic gene. A fragment of the TM DNA proximal to C2, called D1.1, encodes amino acids 9 to 20 of the TM. The DNA sequence and primary amino acid peptide sequence of D1.1 are shown in Table V, SEQ ID NO:10 and SEQ ID NO:20. D1.1 encodes the proximal amino acids of the TM Core polypeptide (residues 12 to 20) as well as a short peptide of three amino acids which serve to join the TM Core with a leader peptide (appropriate for the expression system employed for synthesis of TM). D1.1 is generated by annealing oligonucleotides 1.1 (SEQ ID NO:48) and 2.1 ~~(SEQ ID NO:51)~~ **(SEQ ID NO: 49)** into a DNA duplex as described in Method 1. Oligonucleotides 1.1 and 2.1 have overhanging unpaired ends compatible with the unpaired ends of BamHI (or Bgl II) and Xba I, respectively. D1.1 is annealed into pTMC at the BamHI and Xba I restriction endonuclease sites of the multiple cloning region and the DNA fragments enzymatically ligated, in a manner similar to that described in Method 1 for pTMC, to form the vector pTMD1.1C.

Please replace Paragraph 155 with the following replacement paragraph.

[0155] From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

Summary of Sequence Listing

SEQ ID NO:1 is amino acid sequence of human J chain

SEQ ID NO:2 is amino acid sequence of mouse J chain

SEQ ID NO:3 is amino acid sequence of rabbit J chain

SEQ ID NO:4 is amino acid sequence of bovine J chain

SEQ ID NO:5 is amino acid sequence of bull frog J chain

SEQ ID NO:6 is amino acid sequence of earth worm J chain

SEQ ID NO:7 is nucleotide sequence of "full length" TM cDNA (Table II)

SEQ ID NO:8 is nucleotide sequence of Core TM cDNA (Table VIII)

SEQ ID NO:9 is nucleotide sequence of C2 fragment (Table IV)

SEQ ID NO:10 is nucleotide sequence of D1.1 fragment (Table V)

SEQ ID NO:11 is nucleotide sequence of L3D fragment (Table VI)

SEQ ID NO:12 is nucleotide sequence of T4 fragment (Table VII)

SEQ ID NO:13 is nucleotide sequence of Core TM cDNA using L3 (Table IX)

SEQ ID NO:14 is nucleotide sequence of L3 fragment (Table VI.A)

SEQ ID NO:15 is nucleotide sequence of D1 fragment (Table V.A)

SEQ ID NO:16 is nucleotide sequence of TpS2 (Table X)

SEQ ID NO:17 is amino acid sequence of "full length" TM cDNA (Table II)

SEQ ID NO:18 is amino acid sequence of Core TM cDNA ~~(Table VII)~~ **(Table VIII)**

SEQ ID NO:19 is amino acid sequence of C2 fragment (Table IV)

SEQ ID NO:20 is amino acid sequence of D1.1 fragment (Table V)

SEQ ID NO:21 is amino acid sequence of L3D fragment (Table VI)

SEQ ID NO:22 is amino acid sequence of T4 fragment (Table VII)

SEQ ID NO:23 is amino acid sequence of Core TM cDNA using L3 (Table IX)

SEQ ID NO:24 is amino acid sequence of L3 fragment (Table VI.A)

SEQ ID NO:25 is amino acid sequence of D1 fragment (Table V.A)

SEQ ID NO:26 is amino acid sequence of TpS2 (Table X)

SEQ ID NO:27 is complementary nucleotide sequence of "full length" TM cDNA (Table II)

SEQ ID NO:28 is complementary nucleotide sequence of Core TM cDNA (Table VIII)

SEQ ID NO:29 is complementary nucleotide sequence of C2 fragment (Table IV)

SEQ ID NO:30 is complementary nucleotide sequence of D1.1 fragment (Table V)

SEQ ID NO:31 is complementary nucleotide sequence of L3D fragment (Table VI)

SEQ ID NO:32 is complementary nucleotide sequence of T4 fragment (Table VII)

SEQ ID NO:33 is complementary nucleotide sequence of Core TM cDNA using L3 (Table IX)

SEQ ID NO:34 is complementary nucleotide sequence of L3 fragment (Table VI.A)

SEQ ID NO:35 is complementary nucleotide sequence of D1 fragment (Table V.A)

SEQ ID NO:36 is complementary nucleotide sequence of TpS2 (Table X)

SEQ ID NO:37 is Domain 1, 13 amino acid peptide with substantial β-sheet character

SEQ ID NO:38 is peptide recognized by the tobacco etch virus protease Nia

SEQ ID NO:39 is amino acid residues from pro-cathepsin E

SEQ ID NO:40 is linker from procathepsin

SEQ ID NO:41 is linker from polyimmunoglobulin receptor

SEQ ID NO:42 is nucleotide sequence of secretion signal from pMelBac

SEQ ID NO:43 is amino acid sequence of secretion signal from pMelBac

SEQ ID NO:44 is endomembrane retention signal

SEQ ID NO:45 is residues 585-600 of polyimmunoglobulin receptor

SEQ ID NO:46 is Oligonucleotide 1

SEQ ID NO:47 is Oligonucleotide 2

SEQ ID NO:48 is Oligonucleotide 1.1

SEQ ID NO:49 is Oligonucleotide 1.2

SEQ ID NO:50 is Oligonucleotide 1.2ser

SEQ ID NO:51 is Oligonucleotide 2.2ser

SEQ ID NO:52 is Oligonucleotide 1.2val

SEQ ID NO:53 is Oligonucleotide 2.2val

SEQ ID NO:54 is Oligonucleotide 3

SEQ ID NO:55 is Oligonucleotide 4

SEQ ID NO:56 is Oligonucleotide 5

SEQ ID NO:57 is Oligonucleotide 5.1dg

SEQ ID NO:58 is Oligonucleotide 6

SEQ ID NO:59 is Oligonucleotide 6.1dg

SEQ ID NO:60 is Oligonucleotide 7

SEQ ID NO:61 is Oligonucleotide 8

SEQ ID NO:62 is Oligonucleotide 9

SEQ ID NO:63 is Oligonucleotide 9L3Δ

SEQ ID NO:64 is Oligonucleotide 10L3Δ

SEQ ID NO:65 is Oligonucleotide 9L3ΔKDEL

SEQ ID NO:66 is Oligonucleotide 10L3ΔKDEL

SEQ ID NO:67 is Oligonucleotide 9.2Δ3

SEQ ID NO:68 is Oligonucleotide 10.2Δ3

SEQ ID NO:69 is Oligonucleotide 9.3Δ3/ser68

SEQ ID NO:70 is Oligonucleotide 10.3Δ3/ser68

SEQ ID NO:71 is Oligonucleotide 9.3Δ3/val68

SEQ ID NO:72 is Oligonucleotide 10.3Δ3/val68

SEQ ID NO:73 is Oligonucleotide 10

SEQ ID NO:74 is Oligonucleotide 11

SEQ ID NO:75 is Oligonucleotide 12

SEQ ID NO:76 is Oligonucleotide 13

SEQ ID NO:77 is Oligonucleotide 14

SEQ ID NO:78 is Oligonucleotide 15

SEQ ID NO:79 is Oligonucleotide 16

SEQ ID NO:80 is Oligonucleotide 15KDEL

SEQ ID NO:81 is Oligonucleotide 16KDEL

SEQ ID NO:82 is Oligonucleotide P1

SEQ ID NO:83 is Oligonucleotide P2

SEQ ID NO:84 is nuclear targeting sequence 1

SEQ ID NO:85 is nuclear target sequence 2

SEQ ID NO:86 is HDEL linker sequence for intracellular targeting

SEQ ID NO:87 is Oligonucleotide Tp1

SEQ ID NO:88 is Oligonucleotide Tp2

SEQ ID NO:89 is Oligonucleotide Tp3

SEQ ID NO:90 is Oligonucleotide Tp4

SEQ ID NO:91 is Oligonucleotide Tp5

SEQ ID NO:92 is Oligonucleotide Tp6

SEQ ID NO:93 is synthetic peptide linker

Please replace Table III beginning on page 40, with the following replacement Table III.

-- TABLE III

Oligonucleotides for Construction of Representative Partial TM Genes

OLIGO	SEQUENCE
1:	gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag tgt gct cgt att act t
2:	cta gaa gta ata cga gca cac ttg cac ttg ttg tca acc aga aca ata cgt tca tct tcc t
1.1:	gat cag aag tgc aag tgt gct cgt att act t
2.1:	ct aga agt aat acg agc aca ctt gca ctt ct
1.2ser:	gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag tcc gct cgt att act t
2.2ser:	cta gaa gta ata cga gcg gac ttg cac ttg ttg tca acc aga aca ata cgt tca tct tcc t
1.2val:	gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag gtt gct cgt att act t
2.2val:	cta gaa gta ata cga gca acc ttg cac ttg ttg tca acc aga aca ata cgt tca tct tcc t
3:	cta gaa tca tcc gta gct cag agg acc caa atg aag ata tag tcg aa
4	gat acg gat gtt acg ttc gac tat atc ttc att tgg gtc ctc tga gct acg gat gat t
5:	cgt aac atc cgt atc atc gtc cca ctg aat aac cgg gag aat atc tca g
5.1dg:	cgt aac atc cgt atc atc gtc cca ctg aat aac cgg gag cac atc tca g
6:	acg gac ttg tag gat ctg aga tat tct ccc ggt tat tca gtg gga cga t
6.1dg:	acg gac ttg tag gat ctg aga tgt gct ccc ggt tat tca gtg gga cga t
7:	atc cta caa gtc cgt tgc gca cac gct tcg tat acc acc tgt ca
8:	gat ctg aca ggt ggt ata cga agc gtg tgc gca
9:	gat ctg tgt aag aag tgt gat cca aca gag gta gag ctg gac aat cag ata gtc act gca
9L3Δ:	gat ctg tgt aag aag gat gag gac agc gct aca gaa acc tgc tg
10L3Δ:	aat tca gca ggt ttc tgt agc gct gtc ctc atc ctt ctt aca ca

9L3ΔKDEL: gat ctg tgt aag aag gat gag gac agc gct aca gaa acc tgc tac gag aag gat gag ctg tg

10L3ΔKDEL: aat tca cag ctc atc ctt cgc gtc gca ggt ttc tgt agc gct gtc ctc atc ctt ctt aca ca

9.2Δ3: gat ctg tgt aag aag tct gat atc gat gaa gat tcc gct aca gaa acc tgc agc aca tg

10.2Δ3: aat tca tgt gct gca ggt ttc tgt agc gga atc ttc atc gat atc aga ctt ctt aca ca

9.3Δ3/ser68: gat ctg tct aag aag tct gat atc gat gaa gat tac aga ttc ttc aga cta tag cta ctt cta a

10.3Δ3/ser68: aat ctt cat cga tat cag act tct tag aca

9.3Δ3/val68: gat ctg gtt aag aag tct gat atc gat gaa gat tac caa ttc ttc aga cta tag cta ctt cta a

10.3Δ3/val68: aat ctt cat cga tat cag act tct taa cca

10: att gtc cag ctc tac ctc tgt tgg atc aca ctt ctt aca ca

11: act caa agc aac att tgc gat gag gac agc gct aca gaa acc tgc a

12: ggt ttc tgt agc gct ctg ctc atc gca aat gtt gct ttg agt cgc agt gac tat ctg

13: gc acc tac gat agg aac aaa tgc tac acg gcc gtg gtt ccg ctc gtg tat ggt gga gag

14: gag cgg aac cac ggc cgt gta gca ttt gtt cct atc gta ggt gct gca

15: aca aaa atg gtg gaa act gcc ctt acg ccc gat gca tgc tat ccg gac tg

16: aat tca gtc cgg ata gca tgc atc ggg cgt aag ggc agt ttc cac cat ttt tgt ctc tcc acc ata cac

15KDEL: aca aaa atg gtg gaa act gcc ctt acg ccc gat gca tgc tat ccg gac aag gat gaa ttg tg

16KDEL: aat tca caa ttc atc ctt gtc cgg ata gca tgc atc ggg cgt aag ggc agt ttc cac cat ttt tgt ctc tcc acc ata cac

P1: gat cag gtc gct gcc atc caa gac ccg agg ctg ttc gcc gaa gag aag gcc gtc gct gac tcc aag tgc aag tgt gct cgt att act t

P2: ct aga agt aat acg agc aca ctt gca ctt gga gtc agc gac ggc ctt ctc

ttc ggc gaa cag cct cgg gtc ttg gat ggc agc gac ct

Tp1: gc gat gac gac gat aag gcc caa acg gag acc tgt act gtt gcg cct cgt gaa cgg caa aac tgc gga ttc ccg ~~gaa~~ gga

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Tp2:    gtt ttg ccg ttc acg agg cgc aac agt aca ggt ctc cgt ttg ggc ctt atc
        gtc gtc atc gct ~~tca~~ gca

Tp3:    gta aca ccc tct cag tgc gct aat aaa ggc tgc tgt ttt gat gac acg gta
        cgg ggc gtt ccg tgg tgc ~~ttc~~ ttt

Tp4:    gcc ccg tac cgt gtc atc aaa aca gca gcc ttt att agc gca ctg aga ggg
        tgt tac ~~ttc~~ tcc cgg gaa tcc gca

Tp5:    tac ccc aat aca att gac gtt ccg cct gaa gaa gag tgc gag ccg taa g

Tp6:    aattc tta cgg ctc gca ctc ttc ttc agg cgg caa gtc aat tgt att ggg gta
        ~~gaa~~ aaa gca cca cgg aac
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Please replace Table X beginning on page 49, with the following replacement Table X.

-- Table X

DNA and Primary Amino Acid Sequence of TpS2

```
101 102
cys ser asp asp asp asp lys ala gln thr glu thr cys thr val ala pro
     gc gat gac gac gat aag gcc caa acg gag acc tgt act gtt gcg cct
~~act~~ acg tcg cta ctg ctg cta ttc cgg gtt tgc ctc tgg aca tga caa cgc gga

arg glu arg gln asn cys gly phe pro gly val thr pro ser gln cys ala
cgt gaa cgg caa aac tgc gga ttc ccg ~~gaa~~ gga/gta aca ccc tct cag tgc gct
gca ctt gcc gtt ttg/acg cct aag ggc ~~ctt~~ cct cat tgt ggg aga gtc acg cga

asn lys gly cys cys phe asp asp thr val arg gly val pro trp cys phe
aat aaa ggc tgc tgt ttt gat gac acg gta cgg ggc gtt ccg tgg tgc ~~ttc~~ ttt/
tta ttt ccg acg aca aaa cta ctg tgc cat gcc ccg/caa ggc acc acg ~~aag~~ aaa

tyr pro asn thr ile asp val pro pro glu glu glu cys glu phe
tac ccc aat aca att gac gtt ccg cct gaa gaa gag tgc gag ccg taa g
atg ggg tta tgt taa ctg caa ggc gga ctt ctt ctc acg ctc ggc att cttaa --
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Please replace paragraph [0119] with the following replacement paragraph [0119].

-- [0119] The important properties of the dyes are summarized in Tables ~~X~~ XI and ~~XI~~ XII.

Table ~~X~~ XI

Optical Properties of Cyanine Dyes

Dye	Absorption max. nm (PBS)	E at absorption max.	E280/Emax	Emission max., nm
Cy3.18	550	150,000	0.05	565
Cy5.18	652	250,000	0.05	667
Cy5.5.18	674	250,000	0.08	694

Table ~~XI~~ XII

Molar Relaxivities $1/T1(mMs)^{-1}$ of Paramagnetic Compounds

Compound	Relaxation rate
MnTPPS4	10.39*
MnCl2	9.32*
MriDTP A	6.93*
GdCl	14.67*
GDDTP A	5.05*
MnPcS4	10.10

*$1/T1\ (mMs)^{-1}$, in water at 10.7 MHz, 37°C. --